When coding matters: why the development of outbreak analytics tools needs to be valued, supported, and funded

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MAIN TEXT

The COVID-19 pandemic has brought infectious disease modelling to the forefront, with mainstream media uncovering the good, the bad, and sometimes the ugly in a field of research utilized more than ever for informing public health decision-making. A dramatic example lies in the code release of Imperial College's COVID-19 simulations, which sparked waves of criticisms for its poor coding practices, although results themselves were later found to be reproducible (1).

Does good coding matter in science? If by 'good coding' we mean using practices which make the code clear, easy to reuse, maintain, expand on, and test - in short, reliable - then the answer is yes. And it matters even more when the corresponding piece of software is used to inform public health operations. Unfortunately, scientific software development has struggled to gain recognition (2,3) and there has been little incentive so far for academic researchers to make code free and transparent in infectious disease modelling.

The issue goes beyond modelling. The emergence of *outbreak analytics* as a new field of research emphasizes the need for high-quality, free and open-source software tools for informing the response to infectious disease outbreaks, from data collection to advanced statistical analyses (4).

The issue is not new. Development of tools for outbreak analytics has been chronically under-valued and under-funded. Despite the emergence of initiatives like the R Epidemics Consortium (5) to promote open-source software for outbreak response, such projects typically fall 'between the boxes' of health research funders, lying somewhere between theoretical modelling work and interventions.

As a result, we have faced an absurd situation where data scientists involved in outbreak responses have encountered the same issues at every new outbreak, without ever being able to focus on developing software tools to solve these problems once and for all. While it is frustrating to see this issue finally acknowledged during the biggest public health crisis in recent times, it is not too late for a cultural shift to take place.

Solutions are simple. The development of high-quality scientific software must be valued as other academic outputs. Dedicated career profiles for scientific software engineers must be created to build long-term capacity in academic institutions. Last, and perhaps most importantly, funders need to lead - not follow - this cultural shift, by acknowledging the development of outbreak analytics tools as a field deserving recognition and support.

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